Glu Gly Tyr Gln Ser Ser Gly Thr Ser Ser Ile Asn Val Gly Gly
180 185 190

<210> 11
<211> 191
<212> PRT
<213> Streptomyces lividans
<400> 11

Ala Thr Thr Ile Thr Thr Asn Gln Thr Gly Thr Asp Gly Met Tyr Tyr
1 5 10 15

Ser Phe Trp Thr Asp Gly Gly Gly Ser Val Ser Met Thr Leu Asn Gly
20 25 30

Gly Gly Ser Tyr Ser Thr Gln Trp Thr Asn Cys Gly Asn Phe Val Ala
35 40 45

Gly Lys Gly Trp Ser Thr Gly Asp Gly Asn Val Arg Tyr Asn Gly Tyr
50 55 60

Phe Asn Pro Val Gly Asn Gly Tyr Gly Cys Leu Tyr Gly Trp Thr Ser
65 70 75 80

Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg
85 90 95

Pro Thr Gly Thr Tyr Lys Gly Thr Val Ser Ser Asp Gly Gly Thr Tyr
100 105 110

Asp Ile Tyr Gln Thr Thr Arg Tyr Asn Ala Pro Ser Val Glu Gly Thr
115 120 125

Lys Thr Phe Gln Gln Tyr Trp Ser Val Arg Gln Ser Lys Val Thr Ser
130 135 140

Gly Ser Gly Thr Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Arg
145 150 155 160

Ala Gly Met Asn Met Gly Gln Phe Arg Tyr Tyr Met Ile Asn Ala Thr
165 170 175

Glu Gly Tyr Gln Ser Ser Gly Ser Ser Asn Ile Thr Val Ser Gly
180 185 190

<210> 12
<211> 189
<212> PRT
<213> Streptomyces sp.
<400> 12

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Ala Thr Thr Ile Thr Asn Glu Thr Gly Tyr Asp Gly Met Tyr Tyr Ser
 1               5                  10                  15

Phe Trp Thr Asp Gly Gly Gly Ser Val Ser Met Thr Leu Asn Gly Gly
            20                  25                  30

Gly Ser Tyr Ser Thr Arg Trp Thr Asn Cys Gly Asn Phe Val Ala Gly
        35                  40                  45

Lys Gly Trp Ala Asn Gly Gly Arg Arg Thr Val Arg Tyr Thr Gly Trp
    50                  55                  60

Phe Asn Pro Ser Gly Asn Gly Tyr Gly Cys Leu Tyr Gly Trp Thr Ser
65                  70                  75                  80

Asn Pro Leu Val Glu Tyr Tyr Ile Val Asp Asn Trp Gly Ser Tyr Arg
                85                  90                  95

Pro Thr Gly Glu Thr Arg Gly Thr Val His Ser Asp Gly Gly Thr Tyr
            100                 105                 110

Asp Ile Tyr Lys Thr Thr Arg Tyr Asn Ala Pro Ser Val Glu Ala Pro
        115                 120                 125

Ala Ala Phe Asp Gln Tyr Trp Ser Val Arg Gln Ser Lys Val Thr Ser
    130                 135                 140

Gly Thr Ile Thr Thr Gly Asn His Phe Asp Ala Trp Ala Arg Ala Gly
145                 150                 155                 160

Met Asn Met Gly Asn Phe Arg Tyr Tyr Met Ile Asn Ala Thr Glu Gly
                165                 170                 175

Tyr Gln Ser Ser Gly Ser Ser Thr Ile Thr Val Ser Gly
            180                 185
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<210> 13
<211> 189
<212> PRT
<213> Thermomonospora fusca
<400> 13

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Ala Val Thr Ser Asn Glu Thr Gly Tyr His Asp Gly Tyr Phe Tyr Ser
 1               5                  10                  15

Phe Trp Thr Asp Ala Pro Gly Thr Val Ser Met Glu Leu Gly Pro Gly
            20                  25                  30

Gly Asn Tyr Ser Thr Ser Trp Arg Asn Thr Gly Asn Phe Val Ala Gly
        35                  40                  45
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Lys Gly Trp Ala Thr Gly Gly Arg Arg Thr Val Thr Tyr Ser Ala Ser
50 55 60

Phe Asn Pro Ser Gly Asn Ala Tyr Leu Thr Leu Tyr Gly Trp Thr Arg
65 70 75 80

Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Ser Trp Gly Thr Tyr Arg
85 90 95

Pro Thr Gly Thr Tyr Met Gly Thr Val Thr Thr Asp Gly Gly Thr Tyr
100 105 110

Asp Ile Tyr Lys Thr Thr Arg Tyr Asn Ala Pro Ser Ile Glu Gly Thr
115 120 125

Arg Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Ser Lys Arg Thr Ser
130 135 140

Gly Thr Ile Thr Ala Gly Asn His Phe Asp Ala Trp Ala Arg His Gly
145 150 155 160

Met His Leu Gly Thr His Asp Tyr Met Ile Met Ala Thr Glu Gly Tyr
165 170 175

Gln Ser Ser Gly Ser Ser Asn Val Thr Leu Gly Thr Ser
180 185

<210> 14
<211> 190
<212> PRT
<213> Trichoderma harzianum
<400> 14

Gln Thr Ile Gly Pro Gly Thr Gly Tyr Ser Asn Gly Tyr Tyr Tyr Ser
1 5 10 15

Tyr Trp Asn Asp Gly His Ala Gly Val Thr Tyr Thr Asn Gly Gly Gly
20 25 30

Gly Ser Phe Thr Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Ile Tyr Gly Trp Ser
65 70 75 80

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110

Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140

Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160

Ser His Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175

Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 15
<211> 178
<212> PRT
<213> Trichoderma reesei
<400> 15

Ala Ser Ile Asn Tyr Asp Gln Asn Tyr Gln Thr Gly Gly Gln Val Ser
1 5 10 15

Tyr Ser Pro Ser Asn Thr Gly Phe Ser Val Asn Trp Asn Thr Gln Asp
20 25 30

Asp Phe Val Val Gly Val Gly Trp Thr Thr Gly Ser Ser Ala Pro Ile
35 40 45

Asn Phe Gly Gly Ser Phe Ser Val Asn Ser Gly Thr Gly Leu Leu Ser
50 55 60

Val Tyr Gly Trp Ser Thr Asn Pro Leu Val Glu Tyr Tyr Ile Met Glu
65 70 75 80

Asp Asn His Asn Tyr Pro Ala Gln Gly Thr Val Lys Gly Thr Val Thr
85 90 95

Ser Asp Gly Ala Thr Tyr Thr Ile Trp Glu Asn Thr Arg Val Asn Glu
100 105 110

Pro Ser Ile Gln Gly Thr Ala Thr Phe Asn Gln Tyr Ile Ser Val Arg
115 120 125

Asn Ser Pro Arg Thr Ser Gly Thr Val Thr Val Gln Asn His Phe Asn
130 135 140

Trp Ala Ser Leu Gly Leu His Leu Gly Gln Met Met Asn Tyr Gln Val
145 150 155 160

Val Ala Val Glu Gly Trp Gly Gly Ser Gly Ser Ala Ser Gln Ser Val
165 170 175

Ser Asn

<210> 16
<211> 190
<212> PRT
<213> Trichoderma reesei
<400> 16

Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15

Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30

Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110

Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140

Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160

Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175

Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 17
<211> 190
<212> PRT

<213> Trichoderma viride
<400> 17

Gln Thr Ile Gln Pro Gly Thr Gly Phe Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15

Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30

Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly
50 55 60

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110

Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Thr His
130 135 140

Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160

Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175

Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 18
<211> 586
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX synthetic sequence
<400> 18

ctagctaagg aggctgcaga tgcaaacaat acaaccagga accggttaca acaacggtta 60
cctttacagc tactggaacg atggccatgg tggtgttacc tatacaaacg ggcccggagg 120
ccaatttagc gtcaattggt ctaactccgg aaacttcgta ggtggaaaag gttggcaacc 180
cgggaccaaa aataaggtga tcaacttctc tggatcttat aatccgaatg ggaattcata 240
cttaagcgtc tatggctggt ctagaaaccc actgattgaa tattacattg tcgaaaattt 300
cggtacctac aatccgagta ccggcgccac aaaattaggc gaagtcacta gtgatggatc 360
cgtatatgat atccaccgta cccaacgcgt taatcagcca tcgatcattg gaaccgccac 420
cttttatcag tactggagtg ttagacgtaa tcateggagc tccggttcgg ttaatactgc 480
gaatcacttt aatgcatggg cacagcaagg gttaacccta ggtacaatgg attatcaaat 540
cgtagcggtg gaaggctact tctcgagtgg ttccgctagt attacagtga gctaaa 596

<210> 19
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Trx-110C Synthetic Sequence
<400> 19
atatacggat ccatcacaag tgacttcgcc taatttgtg 40
<210> 20
<211> 68
<212> DNA.
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-110C-2
<400> 20

gcgccacaaa attaggcgaa gtcacttgtg atggatccgt atatgatatc taccgtaccc 60
aacgcgtt 68

<210> 21
<211> 42
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-103b
<400> 21
aatcagccat cgatcattgg aaccgccacc tttatcagt ac 42
<210> 22
<211> 54
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-109
Synthetic sequence
<400> 22
ggtggcggtt ccaatgatcg atggctgatt aacgcgttgg gtacggtaga tatc 54
<210> 23
<211> 48
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108b
<400> 23
cgaaccggag ctccgatgat tacgtctaac actccagtac tgataaaa 48

<210> 24
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-154C
Synthetic sequence
<400> 24
ctagggttaa ccctgtgat gcccaggcat taaagtggca tgcagtatta ac 52
<210> 25
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-154C-2
<400> 25

tggagtgtta gacgtaatca tcggagctcc ggttcggtta atactgcatg ccactttaat 60
gcctgggcac agcaagggtt aacc 84

<210> 26
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-162H-3
<400> 26
ccacttcaat gcatgggcac agcacgggtt aacc 34
<210> 27
<211> 42
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-4
<400> 27
ctagggttaa cccgtgctgt gcccatgcat tgaagtggca tg 42
<210> 28
<211> 58
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-101
<400> 28
tcgacaattt cggtacctac aatccgagca ccggcgccac aaaattaggc gaagtcac 58
<210> 29
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence :XyTv-102
<400> 29
tagtgatgga tccgtatatg atatctaccg tacccaacgc gttaatcagc ca 52
<210> 30
<211> 60
<212> DNA
<213> Artificial Sequence
<220>

<223> Description of Artificial Sequence:TrX-103
<400> 30
tcgatcattg gaaccgccac cttttatcag tactggagtg ttagacgtaa tcatcggagc 60
<210> 31
<211> 69
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-104
<400> 31

tccggttcgg ttaatactgc gaatcacttt aatgcatggg cacagcaagg gttaacccta 60
ggtacaatg 69

<210> 32
<211> 67
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-105
<400> 32

gattatcaaa tcgtagcggt ggaaggctac ttctcgagtg gttccgctag tattacagtg 60
agctaaa 67

<210> 33
<211> 53
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-106 synthetic sequence
<400> 33
gatctttagc tcactgtaat actagcggaa ccactcgaga agtagccttc cac 53
<210> 34
<211> 66
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-107
<400> 34

cgctacgatt tgataatcca ttgtacctag ggttaaccct tgctgtgccc atgcattaaa 60
gtgatt 66

<210> 35
<211> 60
<212> DNA
<213> Artificial Sequence.
<220>
<223> Description of Artificial Sequence:TrX-108
<400> 35
cgcagtatta accgaaccgg agctccgatg attacgtcta acactccagt actgataaaa 60
<210> 36
<211> 73
<212> DNA

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-110
<400> 36

atatacggat ccatcactag tgacttcgcc taattttgtg gcgccggtac tcggattgta 60
ggtaccgaaa ttg 73

<210> 37
<211> 76
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-1
<400> 37

ctagctaagg aggctgcaga tgcaaacaat acaaccagga accggttaca acaacggtta 60
cttttacagc tattgg 76

<210> 38
<211> 78
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-2
<400> 38

aacgatggcc atggtggtgt tacctataca aacgggcccg gaggccaatt tagcgtcaat 60
tggtctaact ccggaaac 78

<210> 39
<211> 78
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-3
<400> 39

ttcgtaggtg gaaaaggttg gcaacccggg accaaaaata aggtgattaa cttctctgga 60
tcttataatc cgaatggg 78

<210> 40
<211> 74
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-4
<400> 40

aattcatact taagcgtcta tggctggtct agaaacccac tgattgaata ttacattgtc 60
gaaaatttcg gtac 74

<210> 41
<211> 85
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence :XyTv-5
<400> 41

gcaaattttc gacaatgtaa tatttaatca gtgggtttct agaccagcca tagacgctta 60
agtatgaatt cccattcgga ttata 85

<210> 42
<211> 78
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Trx-6Synthetic sequence
<400> 42

agatccagag aagttgatca cctttatttt ggtcccgggt tgccaacctt ttccacctac 60
gaagtttccg gagttaga 78

<210> 43
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:XyTv-7
Synthetic sequence
<400> 43

ccaattgacg ctaaattggc ctccgggccc gtttgtatag gtaacaccac catggccatc 60
gttccaatag ctgtaaaagt aacc 84

<210> 44
<211> 51
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-8 synthetic
sequence
<400> 44
gttgttgtaa ccggttcctg gttgtattgt ttgcatctgc agcctcctta g 51
<210> 45
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108C
synthetic sequence
<400> 45
atatacggat ccatcactag tgcattcgcc taattttgtg 40
<210> 46
<211> 68

<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108C-2
<400> 46

gcgccacaaa attaggcgaa tgcactagtg atggatccgt atatgatatc taccgtaccc 60
aacgcgtt 68

<210> 47
<211> 52
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-158C-162H
synthetic sequence
<400> 47
ctagggttaa cccgtgtgat gcccagcaat taaagtgatt tgcagtatta ac 52

<210> 48
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TX-158C-162H-2
<400> 48

tggagtgtta gacgtaatca tcggagctcc ggttcggtta atactgcaaa tcactttaat 60
tgctgggcac agcacgggtt aacc 84

<210> 49
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108c-110c
synthetic seqeuence
<400> 49
atatacggat ccatcacaag tgcattcgcc taattttgtg 40

<210> 50
<211> 68
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:Tx-108C-110C-2
synthetic sequence
<400> 50

gcgccacaaa attaggcgaa tgcacttgtg atggatccgt atatgatatc taccgtaccc 60
aacgcgtt 68

<210> 51
<211> 52
<212> DNA
<213> Artificial Sequence
<220>

<223> Description of Artificial
Sequence:Tx-154C-15SC-152H synthetic seqeunce
<400> 51
ctagggttaa cccgtgtgat gcccagcaat taaegtggca tgcagtatta ac 52

<210> 52
<211> 84
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial
Sequence:Tx-154C-158C-162H-2
<400> 52

tggagtgtta gacgtaatca tcggagctcc ggttcggtta atactgcatg ccactttaat 60
tgctgggcac agcacgggtt aacc 84

<210> 53
<211> 190
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: TrX amino acid
sequence
<400> 53.

Gln Thr Ile Gln Pro Gly Thr Gly Tyr Asn Asn Gly Tyr Phe Tyr Ser
1 5 10 15

Tyr Trp Asn Asp Gly His Gly Gly Val Thr Tyr Thr Asn Gly Pro Gly
20 25 30

Gly Gln Phe Ser Val Asn Trp Ser Asn Ser Gly Asn Phe Val Gly Gly
35 40 45

Lys Gly Trp Gln Pro Gly Thr Lys Asn Lys Val Ile Asn Phe Ser Gly

50 55 60

Ser Tyr Asn Pro Asn Gly Asn Ser Tyr Leu Ser Val Tyr Gly Trp Ser
65 70 75 80

Arg Asn Pro Leu Ile Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr
85 90 95

Asn Pro Ser Thr Gly Ala Thr Lys Leu Gly Glu Val Thr Ser Asp Gly
100 105 110

Ser Val Tyr Asp Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile
115 120 125

Ile Gly Thr Ala Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His
130 135 140

Arg Ser Ser Gly Ser Val Asn Thr Ala Asn His Phe Asn Ala Trp Ala
145 150 155 160

Gln Gln Gly Leu Thr Leu Gly Thr Met Asp Tyr Gln Ile Val Ala Val
165 170 175

Glu Gly Tyr Phe Ser Ser Gly Ser Ala Ser Ile Thr Val Ser
180 185 190

<210> 54
<211> 198
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-DS1 cassette
<400> 54

gcgccacaaa attaggcgaa gtcacttgtg atggatccgt atatgatatc taccgtaccc 60
aacgcgttaa tcagccatcg atcattggaa ccgccaccct ttatcagtac tggagtgtta 120
gacgtaatca tcggagctcc ggttcggtta atactgcatg ccactttaat gcctgggcac 180
agcaagggtt aaccctag 198

<210> 55
<211> 67
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial sequence:TrX-DS1 cassette aa

<400> 55
Gly Ala Thr Lys Leu Gly Glu Val Thr Cys Asp Gly Ser Val Tyr Asp
1 5 10 15

Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
20 25 30

Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
35 40 45

Ser Val Asn Thr Ala Cys His Phe Asn Ala Trp Ala Gln Gln Gly Leu
50 55 60

Thr Leu Gly
65

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS1 cassette aa
<400> 56

Ala Cys His Phe Asn Ala Trp Ala Gln His Gly Leu Thr Leu Gly
1 5 10 15

<210> 57
<211> 198
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS2 cassette
<400> 57

gcgccacaaa attaggcgaa tgcactagtg atggatccgt atatgatatc taccgtaccc 60
aacgcgttaa tcagccatcg atcattggaa ccgccacctt ttatcagtac tggagtgtta 120
gacgtaatca tcggagctcc ggttcggtta atactgcaaa tcactttaat tgctgggcac 180
agcacgggtt aaccctag 198

<210> 58
<211> 67
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS2 cassette aa
<400> 58

Gly Ala Thr Lys Leu Gly Glu Cys Thr Ser Asp Ser Ser Val Tyr Asp
1 5 10 15

Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
20 25 30

Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
35 40 45

Ser Val Asn Thr Ala Asn His Phe Asn Cys Trp Ala Gln His Gly Leu
50 55 60

Thr Leu Gly
65

<210> 59
<211> 198
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS4 cassette
<400> 59

gcgccacaaa attaggcgaa tgcacttgtg atggatccgt atatgatatc taccgtaccc 60
aacgcgttaa tcagccatcg atcattggaa ccgccacctt ttatcagtac tggagtgtta 120
gacgtaatca tcggagctcc ggttcggtta atactgcatg ccactttaat tgctgggcac 180
agcacgggtt aaccctag 198

<210> 60
<211> 67
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS4 cassete aa
<400> 60

Gly Ala Thr Lys Leu Gly Glu Cys Thr Cys Asp Gly Ser Val Tyr Asp
1 5 10 15

Ile Tyr Arg Thr Gln Arg Val Asn Gln Pro Ser Ile Ile Gly Thr Ala
20 25 30

Thr Phe Tyr Gln Tyr Trp Ser Val Arg Arg Asn His Arg Ser Ser Gly
35 40 45

Ser Val Asn Thr Ala Cys His Phe Asn Cys Trp Ala Gln His Gly Leu
50 55 60

Thr Leu Gly
65

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:TrX-162H-DS1 cassette
<400> 61
catgccactt caatgcatgg gcacagcacg ggttaaccct ag 42

Claims

1. An isolated Family 11 xylanase comprising at least one intramolecular disulphide bond, and a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering) or its equivalent, said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase II amino acid sequence defined in SEQ ID NO:16, said isolated xylanase exhibiting at least 40% of optimal activity, when compared to wild-type xylanase, from pH 3.5 to pH 6.0, and from 40 to 60°C, and at least 30% of optimal activity after
a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol;
a pre-incubation step for 30 or 60 minutes at 62.5°C in the absence of a stabilizer or
a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer.

2. The isolated xylanase of claim 1, wherein said basic amino acid is selected from the group consisting of lysine, arginine and histidine.

3. The isolated xylanase of claim 2, wherein said basic amino acid is histidine.

4. The isolated xylanase of claim 1 comprising two disulfide bridges.

5. The isolated xylanase of claim 1 selected from the group consisting of TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4, and TrX-DS8.

6. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS1.

7. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS2.

8. The isolated xylanase of claim 5, wherein said xylanase is TrX-162H-DS4.

9. The isolated xylanase of claim 5, wherein said xylanase is TrX-DS8.

10. A method of obtaining Family 11 xylanase comprising:

i) selecting an organism that expresses xylanase activity, and obtaining said xylanase from said organism;
ii) determining whether said xylanase exhibits at least 40% of optimal activity, when compared to wild-type xylanase, from pH 3.5 to pH 6.0, and from 40 to 60°C; and
iii) determining whether said xylanase is a Family 11 xylanase and exhibits at least 30% of optimal activity after

a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol;
a pre-incubation step for 30 or 60 minutes at 62.5°C in the absence of a stabilizer; or
a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer;
iv) determining whether said xylanase has a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering), said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase II amino acid sequence defined in SEQ ID NO: 16, and an intra-molecular disulfide bond; and
v) retaining said xylanase that expresses these properties.

11. The method of claim 10, wherein step i) includes partially purifying said xylanase.

12. A method of preparing animal feed comprising applying the isolated xylanase of claim 1 onto said animal feed to produce a xylanase-animal feed combination, and heat sterilizing said xylanase-animal feed combination.

13. The method of claim 12, wherein said animal feed is a poultry or swine feed.

14. A method of preparing animal feed comprising, applying the xylanase obtained from step v) of claim 10 onto said animal feed to produce a xylanase-animal feed combination, and heat sterilizing said xylanase-animal feed combination.

15. The method of claim 14, wherein said animal feed is a poultry or swine feed.

16. The isolated xylanase of claim 1, wherein the xylanase is recombinant.

17. The isolated xylanase of claim 1 comprising one disulfide bridge.

18. The isolated xylanase of claim 1, said xylanase obtained from an organism selected from the group consisting of *Aspergillus niger, Aspergillus kawachii, Aspergillus tubigensis, Bacillus circulans, Bacillus pumilus, Bacillus subtilis, Cellulomonas fimi, Chainia spp., Clostridium acetobutylicum, Clostridium stercorarium, Fibrobacter succinogenes, Neocallimastorix patriciarum, Nocardiopsis dassonvillei, Ruminococcus flavefaciens, Schizophyllum commune, Streptomyces lividens, Streptomyces sp. No,36a, Streptomyces thermoviolaceus, Thermomonospora fusca, Trichoderma harzianum, Trichoderma reesei,* and *Trichoderma viride.*

19. An isolated Family 11 xylanase characterized in comprising at least one intramolecular disulfide bond, and a basic amino acid at position 162 (*Trichoderma reesei* xylanase II numbering) or its equivalent, said position determined from sequence alignment of said isolated xylanase with said *Trichoderma reesei* xylanase n amino acid sequence defined in SEQ ID NO:16, said xylanase exhibiting at least 30% of optimal activity, when compared to wild-type xylanase, after
a pre-incubation step for 30 minutes at 70°C, 80°C or 90°C in the presence of 40% glycerol;
a pre-incubation step for 30 or 60 minutes at 625°C in the absence of a stabilizer, or
a pre-incubation step of 30 minutes at 64°C or 68°C in the absence of a stabilizer.

Patentansprüche

1. Isolierte Xylanase der Familie 11, umfassend mindestens eine intramolekulare Disulfid-Bindung und eine basische Aminosäure in Position 162 (*Trichoderma reesei* Xylanase II Numerierung) oder deren Äquivalent, wobei diese Position durch Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgelegt wurde, wobei die genannte isolierte Xylanase, im Vergleich mit Xylanase vom Wildtyp, mindestens 40% der optimalen Aktivität im Bereich von pH 3,5 bis 6,0 und von 40 bis 60°C zeigt, und nach
einem 30 minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin,
einem 30- oder 60 minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder
einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators
mindestens 30% der optimalen Aktivität zeigt.

2. Isolierte Xylanase gemäß Anspruch 1, worin die genannte basische Aminosäure ausgewählt ist aus der Gruppe, die aus Lysin, Arginin und Histidin besteht.

3. Isolierte Xylanase gemäß Anspruch 2, worin die genannte basische Aminosäure Histidin ist.

4. Isolierte Xylanase gemäß Anspruch 1, umfassen zwei Disulfid-Brücken.

5. Isolierte Xylanase gemäß Anspruch 1, ausgewählt aus der Gruppe, die aus TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4 und TrX-DS8 besteht.

6. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS1 ist.

7. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS2 ist.

8. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-162H-DS4 ist.

9. Isolierte Xylanase gemäß Anspruch 5, worin die Xylanase TrX-DS8 ist.

10. Verfahren zum Gewinnen einer Xylanase der Familie 11, umfassen:

i) Auswählen eines Organismus', der Xylanase-Aktivität exprimiert, und Gewinnen der Xylanase aus diesem Organismus;
ii) Feststellen, ob diese Xylanase, im Vergleich mit Xylanase vom Wildtyp, mindestens 40% der optimalen Aktivität im Bereich von pH 3,5 bis pH 6,0 und von 40 bis 60°C zeigt;
iii) Feststellen, ob die genannte Xylanase eine Xylanase der Familie 11 ist und nach einem 30 minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin, einem 30- oder 60 minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators mindestens 30% der optimalen Aktivität zeigt;
iv) Feststellen, ob die genannte Xylanase eine basische Aminosäure in Position 162 *(Trichoderma reesei* Xylanase 11 Numerierung), wobei diese Position durch einen Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgestellt wird, und eine intramolekulare Disulfid-Bindung besitzt, und
v) Gewinnen oder Zurückbehalten der Xylanase, die diese Eigenschaften zeigt.

11. Verfahren nach Anspruch 10, worin Schritt i) das teilweisen Reinigen der Xylanase umfasst.

12. Verfahren zum Herstellen von Tierfutter, umfassend das Aufbringen der isolierten Xylanase gemäß Anspruch 1 auf das Tierfutter, um eine Xylanase-Tierfutter-Kombination zu erzeugen, und Hitzesterilisieren der genannten Xylanase-Tierfutter-Kombination.

13. Verfahren gemäß Anspruch 12, worin das Tierfutter ein Geflügel- oder Schweinefutter ist.

14. Verfahren zum Herstellen von Tierfutter, umfassend das Aufbringen der aus Schritt v) des Anspruchs 10 erhaltenen Xylanase auf das genannte Tierfutter, um eine Xylanase-Tierfutter-Kombination zu erzeugen, und Hitzesterilisieren der genannten Xylanase-Tierfutter-Kombination.

15. Verfahren nach Anspruch 14, worin das Tierfutter ein Geflügel- oder Schweinefutter ist.

16. Isolierte Xylanase gemäß Anspruch 1, worin die Xylanase rekombinant ist.

17. Isolierte Xylanase gemäß Anspruch 1, umfassend eine (einzige) Disulfid-Brücke.

18. Isolierte Xylanase gemäß Anspruch 1, worin die Xylanase aus einem Organismus gewonnen wurde, der ausgewählt ist aus der aus *Aspergillus niger, Aspergillus kawachii, Aspergillus tubigensis, Bacillus circulans, Bacillus pumilus, Bacillus subtilis, Cellulomonas fimi, Chainia spp., Clostridium acetobutylicum, Clostridium stercorarium, Fibrobacter succinogenes, Neocallimastrix patriciarum, Nocardiopsis dassonvillei, Ruminococcus flavefaciens, Schizophyllum commune, Streptomyces lividans, Streptomyces sp. Nr. 36a, Streptomyces thermoviolaceus, Thermomonospora fusca, Trichoderma harzianum, Trichoderma reesei* und *Trichoderma viride* umfassenden Gruppe.

19. Isolierte Xylanase der Familie 11, **dadurch gekennzeichnet, dass** sie mindestens eine intramolekulare Disulfid-

Brücke und und eine basische Aminosäure in Position 162 (*Trichoderma reesei* Xylanase 11 Numerierung) oder deren Äquivalent umfasst, wobei diese Position durch Sequenzvergleich der genannten isolierten Xylanase mit der Aminosäuresequenz der genannten *Trichoderma reesei* Xylanase II, wie sie in SEQ ID NO:16 definiert ist, festgelegt wurde, wobei die genannte Xylanase, im Vergleich mit Xylanase vom Wildtyp, nach einem 30 minütigen Vorinkubations-Schritt bei 70°C, 80°C oder 90°C in der Gegenwart von 40% Glycerin, einem 30- oder 60 minütigen Vorinkubations-Schritt bei 62,5°C in Abwesenheit eines Stabilisators oder einem 30-minütigen Vorinkubations-Schritt bei 64°C oder 68°C in Abwesenheit eines Stabilisators mindestens 30% der optimalen Aktivität zeigt.

Revendications

1. Xylanase isolée de la famille 11 comprenant au moins un pont disulfure intramoléculaire, et un acide aminé basique à la position 162 (numérotation de la xylanase II de *Trichoderma reesei)* ou son équivalent, ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma reesei* définie dans SEQ ID N° : 16, ladite xylanase isolée présentant au moins 40 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage de pH 3,5 à pH 6,0, et de 40 à 60°C, et au moins 30 % d'activité optimale après une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol :
une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou
une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur.

2. Xylanase isolée selon la revendication 1, dans laquelle ledit acide aminé basique est choisi dans le groupe constitué par la lysine, l'arginine et l'histidine.

3. Xylanase isolée selon la revendication 2, dans laquelle ledit acide aminé basique est l'histidine.

4. Xylanase isolée selon la revendication 1, comprenant deux ponts disulfure.

5. Xylanase isolée selon la revendication 1, choisie dans le groupe constitué par TrX-162H-DS1, TrX-162H-DS2, TrX-162H-DS4, et TrX-DS8.

6. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS1.

7. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS2.

8. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-162H-DS4.

9. Xylanase isolée selon la revendication 5, dans laquelle ladite xylanase est TrX-DS8.

10. Procédé d'obtention d'une xylanase de la famille 11, comprenant :

i) la sélection d'un organisme qui exprime l'activité xylanase, et l'obtention de ladite xylanase dudit organisme ;
ii) la détermination du fait que la xylanase présente ou non au moins 40 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage de pH 3,5 à pH 6,0, et de 40 à 60°C ; et
iii) la détermination du fait que ladite xylanase est une xylanase de la famille 11 et présente au moins 30 % d'activité optimale après
une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol ;
une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou
une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur :
iv) la détermination du fait que ladite xylanase a ou non un acide aminé basique à la position 162 (numérotation de la xylanase II de *Trichoderma* reesei), ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma* reesei définie dans SEQ ID N° : 16, et un pont disulfure intramoléculaire ; et
v) la conservation de ladite xylanase qui exprime ces propriétés.

11. Procédé selon la revendication 10, dans lequel l'étape I) comprend la purification partielle de ladite xylanase.

12. Procédé de préparation de nourriture pour animaux comprenant l'application de la xylanase isolée selon la revendication 1 sur ladite nourriture pour animaux pour produire une combinaison de xylanase-nourriture pour animaux, et la stérilisation thermique de ladite combinaison de xylanase-nourriture pour animaux.

13. Procédé selon la revendication 12, dans lequel ladite nourriture pour animaux est de la nourriture pour la volaille ou les porcs.

14. Procédé de préparation de nourriture pour animaux comprenant l'application de la xylanase obtenue dans l'étape v) de la revendication 10 sur ladite nourriture pour animaux pour produire une combinaison xylanase-nourriture pour animaux, et la stérilisation thermique de ladite combinaison de xylanase-nourriture pour animaux.

15. Procédé selon la revendication 14, dans lequel ladite nourriture pour animaux est de la nourriture pour la volaille ou les porcs.

16. Xylanase isolée selon la revendication 1, dans laquelle la xylanase est recombinante.

17. xylanase isolée selon la revendication 1, comprenant un pont disulfure.

18. Xylanase isolée selon la revendication 1, ladite xylanase étant obtenue à partir d'un organisme choisi dans le groupe constitué par *Aspergillus niger*, *Aspergillus kawachii*, *Aspergillus tubigensis*, Bacillus *circulans*, *Bacillus pumilus*, *Bacillus subtilis*, *Cellulomonas fimi*, Chainia spp., *Clostridium acetobutylicum*, *Clostridium stercorarium*, *Fibrobacter succinogenes*, *Neocallimasterix patriciarum*, *Nocardiopsis dassonvillei*, *Ruminococcus flavefaciens*, *Schizophyllum commune*, *Streptomyces lividans*, *Streptomyces sp. No. 36a*, *Streptomyces thermoviolaceus*, *Thermomonospora* fusca, *Trichoderma harzianum*, *Trichoderma reesei*, et *Trichoderma viride*.

19. Xylanase isolée de la famille 11 **caractérisée en ce qu'**elle comprend au moins un pont disulfure intramoléculaire, et un acide aminé basique à la position 182 (numérotation de la xylanase II de *Trichoderma reesei*) ou son équivalent, ladite position étant déterminée à partir de l'alignement de séquence de ladite xylanase isolée avec ladite séquence d'acides aminés de la xylanase II de *Trichoderma* reesei définie dans SEQ ID N° : 16, ladite xylanase isolée présentant au moins 30 % d'activité optimale lorsqu'elle est comparée à la xylanase de type sauvage après
une étape de pré-incubation de 30 minutes à 70°C, 80°C ou 90°C en présence de 40 % de glycérol ;
une étape de pré-incubation de 30 ou 60 minutes à 62,5°C en l'absence d'un stabilisateur ; ou
une étape de pré-incubation de 30 minutes à 64°C ou 68°C en l'absence d'un stabilisateur.

```
                                                                  S AFNTQAAP   31
                                                                  G    1
Ca     23
Cs      1
                                  o
Bp      1  RTITNNEMGN   HSGYDYELWK DYGNT-SMTL NNGGAFSAGW N--NIGNA  45
Ca     32  KTITSNEIGV   NGGYDYELWK DYGNT-SMTL KNGGAFSCQW S--NIGNA  76
Cs      2  RIIYDNETGT   HGGYDYELWK DYGNT-IMEL NDGGTPSCQW S--NIGNA  46
Rf      1  SAADQQTRGN   VGGYDYEMWN QNGQGQASMN PGAGSFTCSW S--NIENF  46
Tr2     1   QTIQPGTGY   NNGYFYSYWN DGHGGVTYTN GPGGQFSVNW S--NSGNF  45
Tv      1   QTIQPGTGF   NNGYPYSYWN DGHGGVTYTN GPGGQFSVNW S--NSGNF  45
Th      1   QTIGPGTGY   SNGYYYSYWN DGHAGVTYTN GGGGSFTVNW S--NSGNF  45
Sc      1   SGTPSSTGT   DGGYYYSWWT DGAGDATYQN NGGGSYTLTW SG-NNGNL  46
An      1           S   AGINYVQNYN GNLGDFTY-D ESAGTFSMYW EDGVSSDF   38
AT      1           S   AGINYVQNYN QNLGDFTY-D ESAGTFSMYW EDGVSSDP   38
Tr1     1               ASINYDQNYQ TGG-QVSYS- PSNTGFSVNW N--TQDDF   34
Ss      1   ATTIT-NETGY D-GMYYSFWT DGGGSVSMTL NGGGSYSTRW T--NCGNF   45
S1B     1   DTVVTTNQEGT NNGYYYSFWT DSQGTVSMNM GSGGQYSTSW R--NTGNF   47
S1C     1   ATTITTNQTGT D-GMYYSFWT DGGGSVSMTL NGGGSYSTQW T--NCGNF   46
Tf      1   AVTSNETGY   HDGYFYSFWT DAPGTVSMEL GPGGNYSTSW R--NTGNF   45
Bc      1               ASTDYWQNWT DGGGIVNAVN GSGGNYSVNW S--NTGNF   36
Bs      1               ASTDYWQNWT DGGGIVNAVN GSGGNYSVNW S--NTGNF   36

Bp     46  LFRK-GKKFD ST-RTHHQLG NISINYNASF N-PSGNSYLC VYGWTQSP   90
Ca     77  LFRK-GKKFN DT-QTYKQLG NISVNYNCNY Q-PYGNSYLC VYGWTSSP   121
Cs     47  LFRK-GRKFN SD-KTYQELG DIVVEYGCDY N-PNGNSYLC VYGWTRNF   91
Rf     47  LARM-GKNYD SQKQNYKAFG NIVLTYDVEY T-PRGNSYMC VYGWTRNP   92
Tr2    46  VGGK-GWQPG TKNKV----- ---INFS-GS YNPNGNSYLS VYGWSRNP   83
Tv     46  VGGK-GWQPG TKNKV----- ---INFS-GS YNPNGNSYLS IYGWSRNP   83
Th     46  VGGK-GWQPG TKNKV----- ---ISYS-GT YQPNGNSYLS VYGWTRSS   84
Sc     47  VGGK-GWNPG AASRS----- ---ITYSAEY SASGSSSYLA VYGWVNYP   76
An     39  VVGL-GWTTG SSNA------ ---ITYSAEY SASGSASYLA VYGWVNYP   77
At     39  VVGLGGWTTG SSNA------ ---INFGGSP SVNSGTGLLS VYGWSTNP   72
Tri    35  VVGV-GWTTG SSAP------ ---VRYT-GW FNPSGNGYGC LYGWTSNP   82
Ss     46  VAGK-GWANG GR-RT----- ---VQYS-GS FNPSGNAYLA LYGWTSNP   84
S1B    48  VAGK-GWANG GR-RT----- ---VRYN-GY FNPVGNGYGC LYGWTSNP   82
S1C    47  VAGK-GWSTG DGN------- ---VRYN-GY FNPSGNAYLT LYGWTRNP   82
Tf     46  VAGK-GWATG GR-RT----- ---VTYS-AS FNPSGNAYLT LYGWTRSP   75
Bc     37  VVGK-GWTTG SPFRT----- ---INYNAGV WAPNGNGYLT LYGWTRSP   75
Bs     37  VVGK-GWTTG SPFRT----- ---INYNAGV WAPNGNGYLT LYGWTRSP   75
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FIGURE 1

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Bp   91  LAEYYIVDSW GTYR-PT--G AYXGSFYADG GTYDIYETTR VNQPSIIG 135
Ca  122  LVEYYVIDSW GSWRPP--GG TSKGTITVDG GIYDIYETTR INQPSIQG 167
Cs   92  LVEYYIVESW GSWRPP--GA TPKGTITQWMAGTYEIYETTR VNQPSIDG 138
Rf   93  LMEYYIVEGW GDWRPPGNDG EVKGTVSANG NTYDIRRTMR YNQPSLDG 140
Tr2  84  LIEYYIVENF GTYN-PSTGA TKLGEVTSDG SVYDIYRTQR VNQPSIIG 130
Tv   84  LIEYYIVENF GTYN-PSTGA TKLGEVTSDG SVYDIYRTQR VNQPSIIG 130
Th   84  LIEYYIVENF GTYN-PSTGA TKLGEVTSDG SVYDIYRTQR VNQPSIIG 130
Sc   85  LIEYYIVESY GSYD-PSSAA SHKGSVTCNG ATYDILSTWR YNAPSIDG 131
An   77  GAEYYIVEDY GDYN-PCSSA TSLGTVYSDG STYQVCTDTR INEPSITG 123
At   78  QAEYYIVEDY GDYN-PCSSA TSLGTVYSDG STYQVCTDTR INEPSITG 124
Trl  73  LVEYYLMEDN HNY--PAQ-G TVKGTVTSDG ATYTIWENTR VNEPSIQG 117
Ss   83  LVEYYIVDNW GSYR-PT--G ETRGTVHSDG GTYDIYKTTR YNKPSVEG 127
S1B  85  LVEYYIVDNW GTYR-PT--G EYKGTVTSDG GTYDIYQTTR YNAPSVEG 129
S1C  83  LVEYYIVDNW GSYR-PT--G TYKGTVSSDG GTYDIYQTTR YNAPSVEG 127
Tf   83  LVEYYIVESW GTYR-PT--G TYMGTVTTDG GTYDIYKTTR YNAPSIEG 127
Bc   76  LIEYYVVDSW GTYR-PT--G TYKGTVKSDG GTYDIYTTTR YNAPSIDG 120
Bs   76  LIEYYVVDSW GTYR-PT--G TYKGTVKSDG GTYDIYTTTR YNAPSIDG 120

Bp  136  -IATPKQYWS VRQTKRTS-- ------GTVS VSAHFRKWES LGMPM-GK 174
Ca  168  -NTTPKQYWS VRRTKRTS-- ------GTIS VSKHFAAWES KGMPL-GK 206
Cs  139  -TATPQQYWS VRTSKRTS-- ------GTIS VTEHFKQWER MGMRM-GK 177
Rf  141  -TATPPQYWS VRQTSGSANN QTNYMKGTID VSKHFDAWSA AGLDMSGT 187
Tr2 131  -TATPYQYWS VRRNHR-S-S ------GSVN TANHFNAWAQ QGLTL-GT 168
Tv  131  -TATPYQYWS VRRTHR-S-S ------GSVN TANHFNAWAS HGLTL-GT 168
Th  131  -TATPYQYWS VRRNHR-S-S ------GSVN TANHFNAWAS HGLTL-GT 168
Sc  132  -TQTPEQFWS VRNPKKAPGG SIS---GTVD VQCHFDAWKG LGMNLGSE 175
An  124  -TSTPTQYFS VRESTRTS-- ------GTVT VANHFNFWAH HGFHN-SD 163
At  125  -TSTPTQYFS VRESTRTS-- ------GTVT VANHFNFWAH HGFHN-SD 163
Trl 118  -TATPNQYIS VRNSPR-T-S ------GTVT VQNHFN-WAS LGLHLGQM 155
Ss  128  -PAAPDQYWS VRQSKVT--S ------GTIT TGNHFDAWAR AGMNMGNF 168
S1B 130  TR-TPDQYWS VRQSKR-TG- ------GTIT TGNHFDAWAR AGMPLGNF 168
S1C 128  TK-TPQQYWS VRQSKVTSGS ------GTIT TGNHFDAWAR AGMNMGQF 168
Tf  128  TR-TPDQYWS VRQSKRTS-- ------GTIT AGNHFDAWAR HGMHLGTH 166
Bc  121  DRTTPTQYWS VRQSKRPTGS N-----ATIT FTNHVNAWKS HGMNLGSN 163
Bs  121  DRTTPTQYWS VRQSKRPTGS N-----ATIT FSNHVNAWKS HGMNLGSN 163
```

FIGURE 1 (CONT'D)

Bp	174	MYETAFTVEG YQSSGSANVM TNQLFIGN	201
Ca	207	MHETAFNIEG YQSSGKADVN SMSINIGK	233
Cs	178	MYEVALTVEG YQSSGYANVY KNEIRIGANP....	
Rf	188	LYEVSLNIEG YRSNGSANVK SVSV	211
Tr2	169	MDYQIVAVEG YFSSGSASI- TVS	190
Tv	169	MDYQIVAVEG YFSSGSASI- TVS	190
Th	169	MDYQIVAVEG YFSSGSASI- TVS	190
Sc	176	HNYQIVATEG YQSSGTATI- TVT	197
An	163	FNYQVMAVEA WSGAGSASV- TISS	184
At	164	FNYQVVAVEA WSGAGSAAV- TISS	185
Tr1	156	MNYQVVAVEG WGGSGSASQ- SVSN	178
Ss	167	RYYMINATEG YQSSGSSTI- TVSG	189
SlB	169	SYYMINATEG YQSSGTSSI- NVGG.....	
SlC	169	RYYMINATEG YQSSGSSNI- TVSG	191
Tf	167	D-YMIMATEG YQSSGSSNVT LGTS.....	
Bc	164	WAYQVMATEG YQSSGSSNV- TVW	185
Bs	164	WAYQVMATEG YQSSGSSNV- TVW	185

Bp *Bacillus pumilus*
Ca *Clostridium acetobutylicum* P262 XynB
Cs *Clostridium stercorarium* xynA
Rf *Ruminococcus flavefaciens*
Tr2 *Trichoderma reesei* XYN II
Tv *Trichoderma viride*
Th *Trichoderma harzianum*
Sc *Schizophyllum commune* Xylanase A
An *Aspergillus niger*, var. *awamori*
At *Aspergillus tubigensis*
Tr1 *Trichoderma reesei* XYN I
Ss *Streptomyces* sp. 36a
SlB *Streptomyces lividans* Xln B
SlC *Streptomyces lividans* Xln C
Tf *Thermomonospora fusca* TfxA
Bc *Bacillus circulans*
Bs *Bacillus subtilis*

FIGURE 1 (CONT'D)

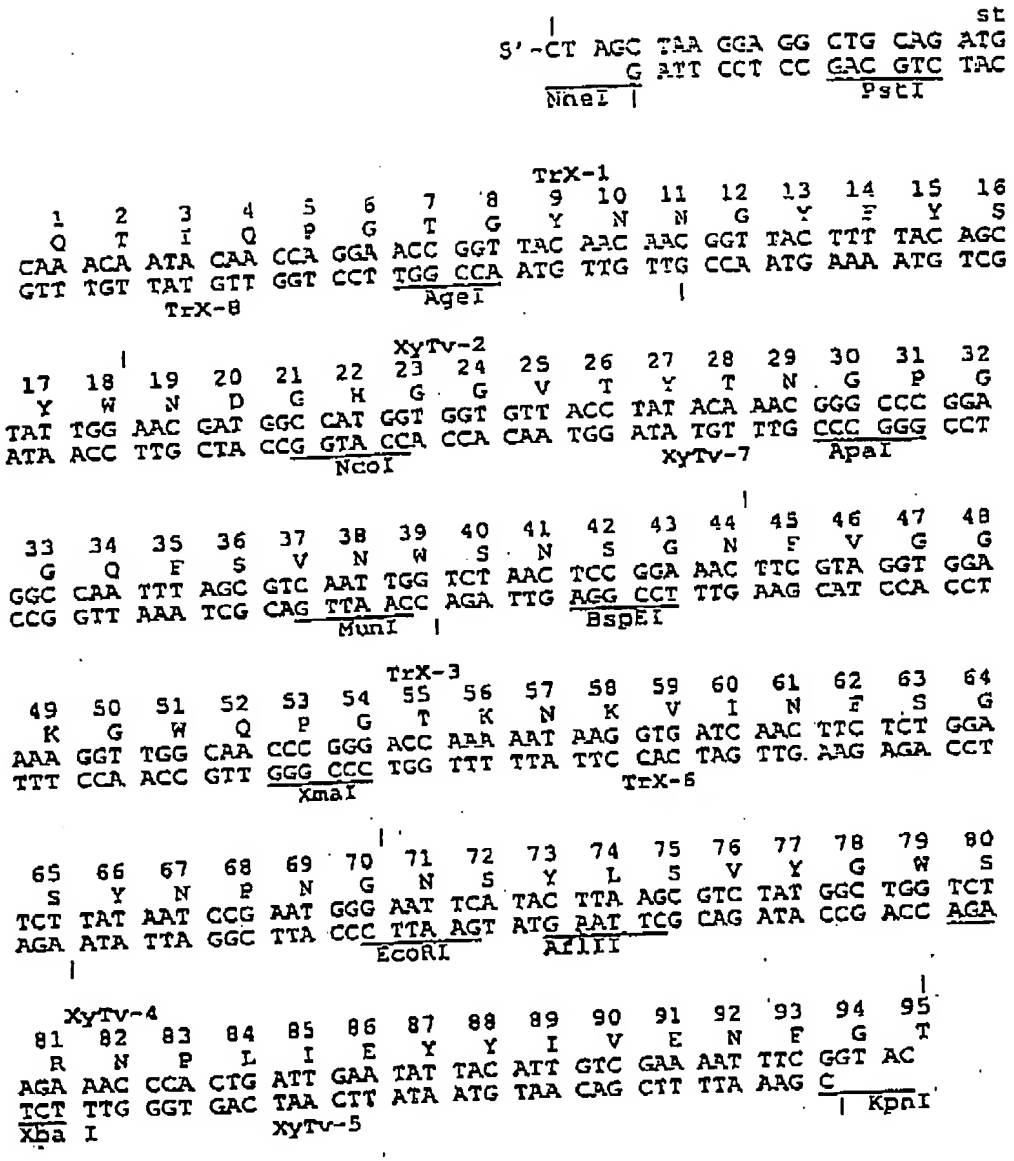

FIG. 2

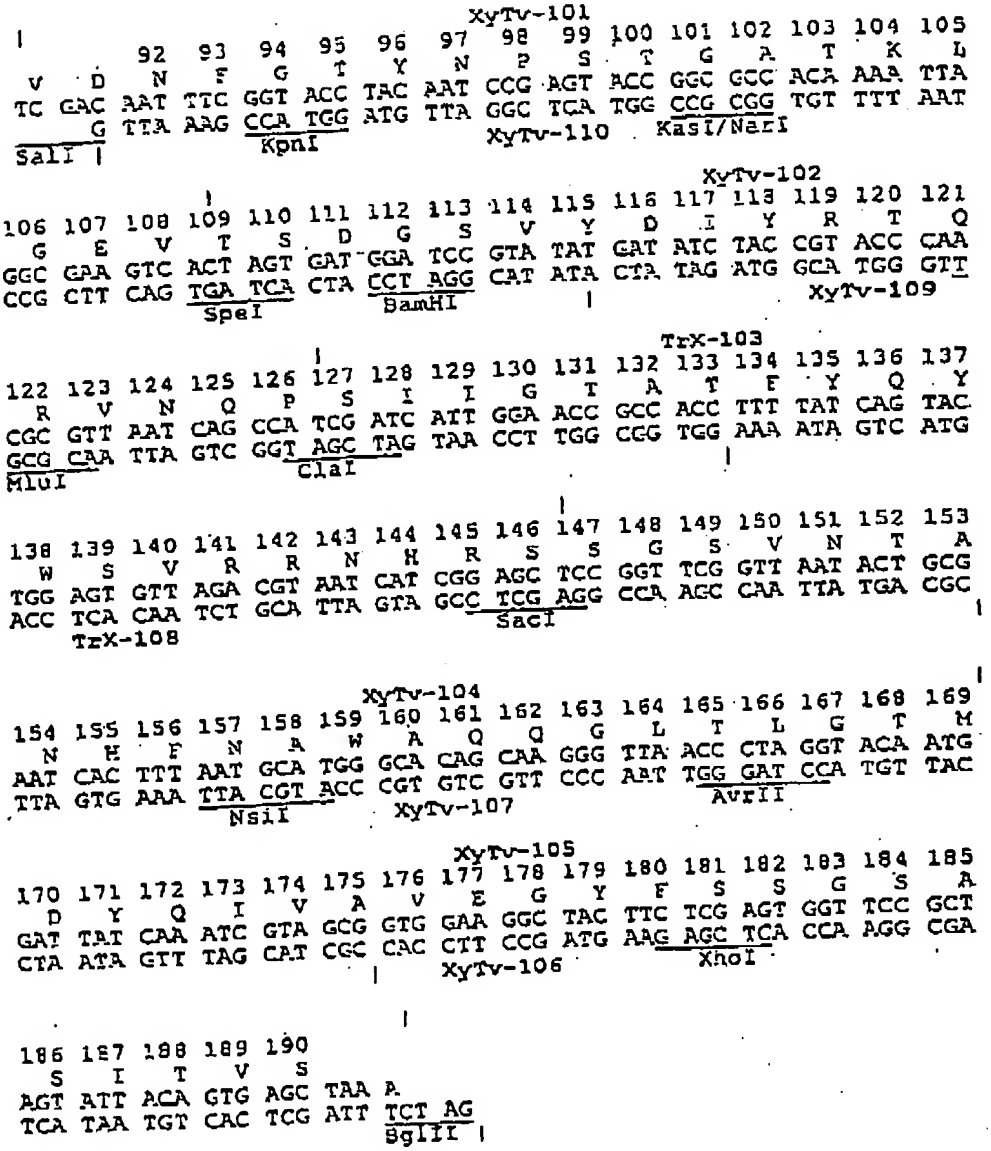
XyTv-101
XyTv-110
KasI/NarI
XyTv-102
XyTv-109
TrX-103
SalI
KpnI
SpeI
BamHI
ClaI
MluI
SacI
TrX-108
XyTv-104
XyTv-107
NsiI
AvrII
XyTv-105
XyTv-106
XhoI
BglII

FIG. 2 (CONT'D)

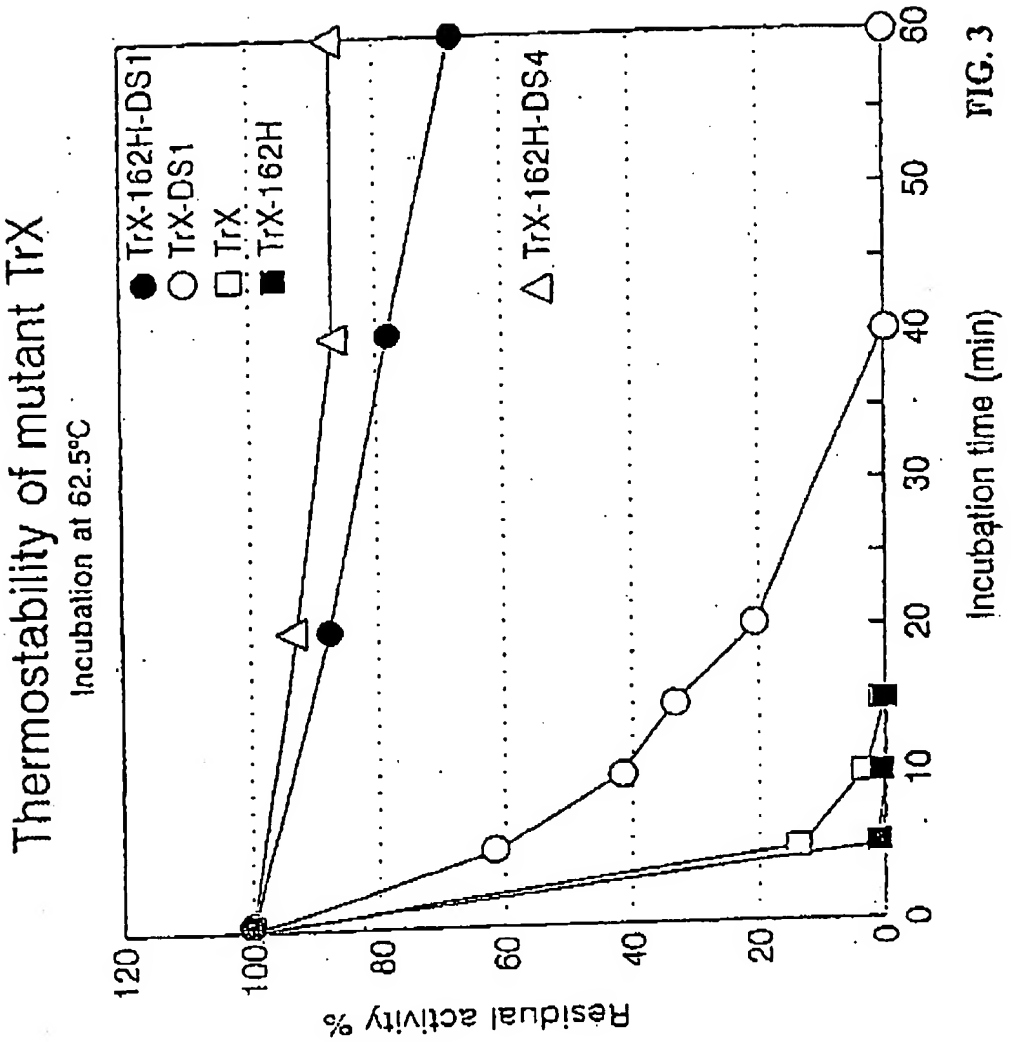

FIG. 3

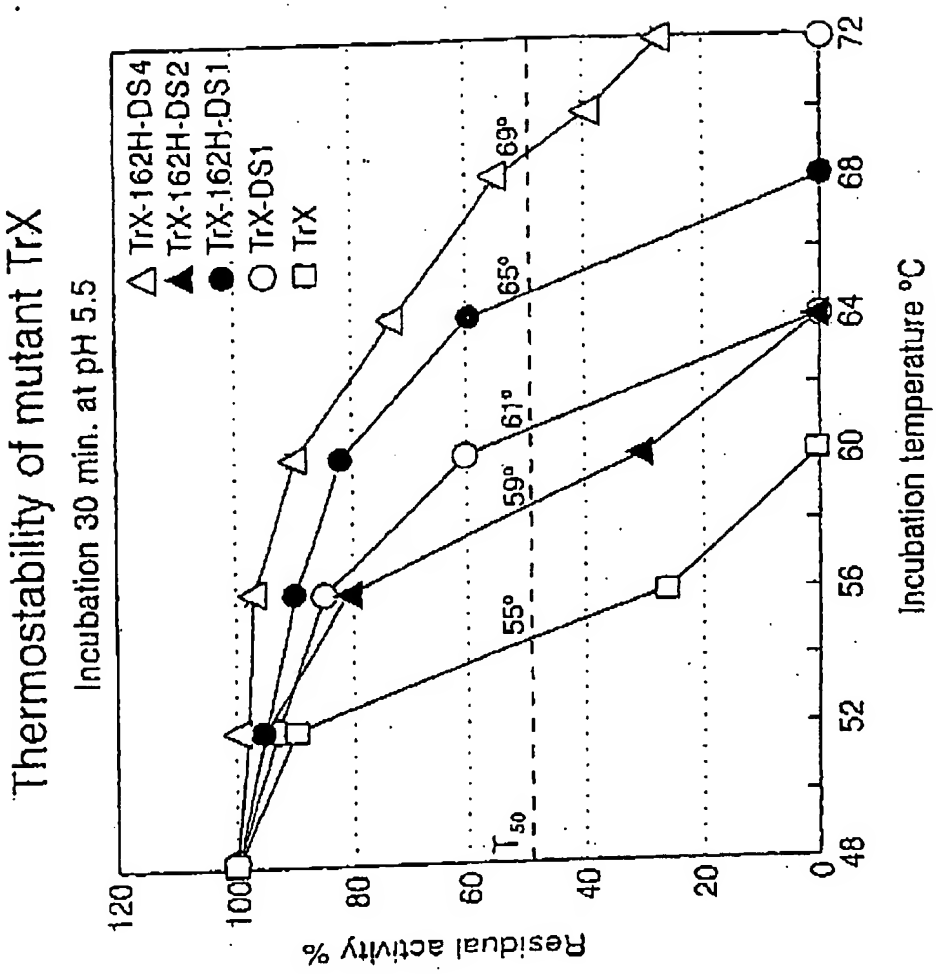
Thermostability of mutant TrX
Incubation 30 min. at pH 5.5
TrX-162H-DS4
TrX-162H-DS2
TrX-162H-DS1
TrX-DS1
TrX
69°
65°
61°
59°
55°
T_{50}
Residual activity %
120
100
80
60
40
20
0
48
52
56
60
64
68
72
Incubation temperature °C

FIG. 4A

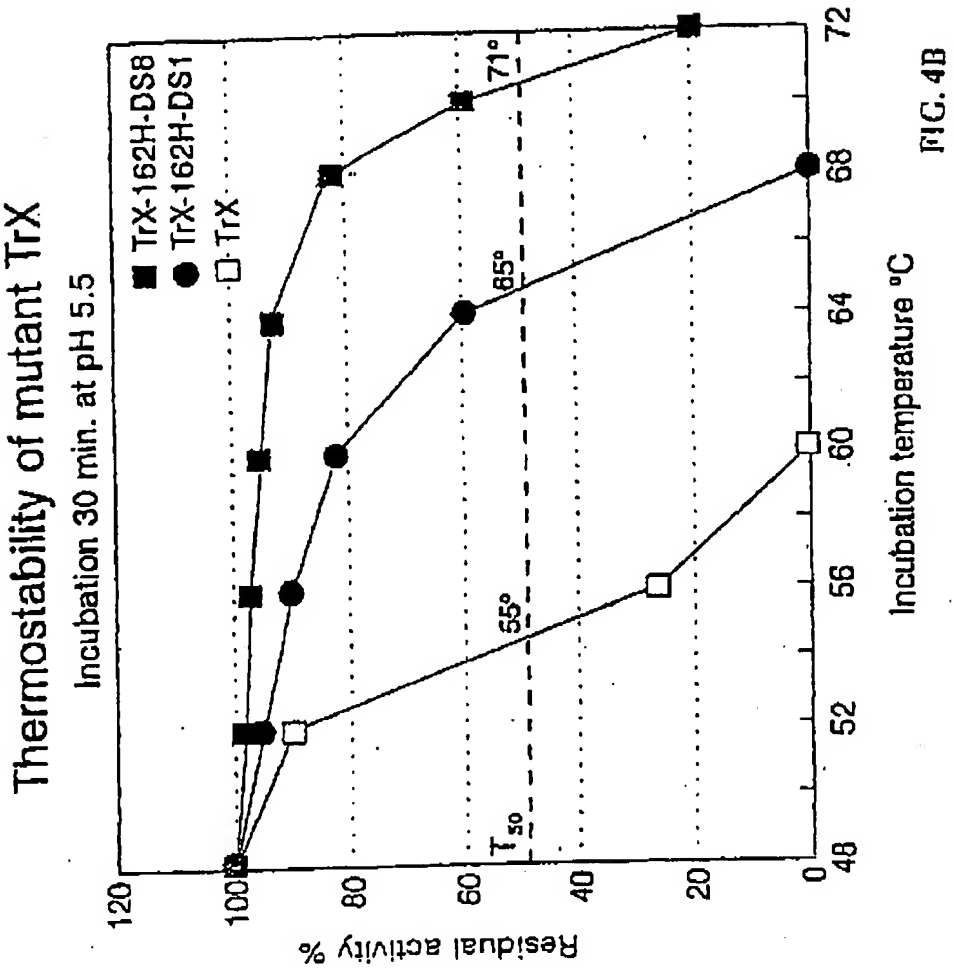

FIG. 4B

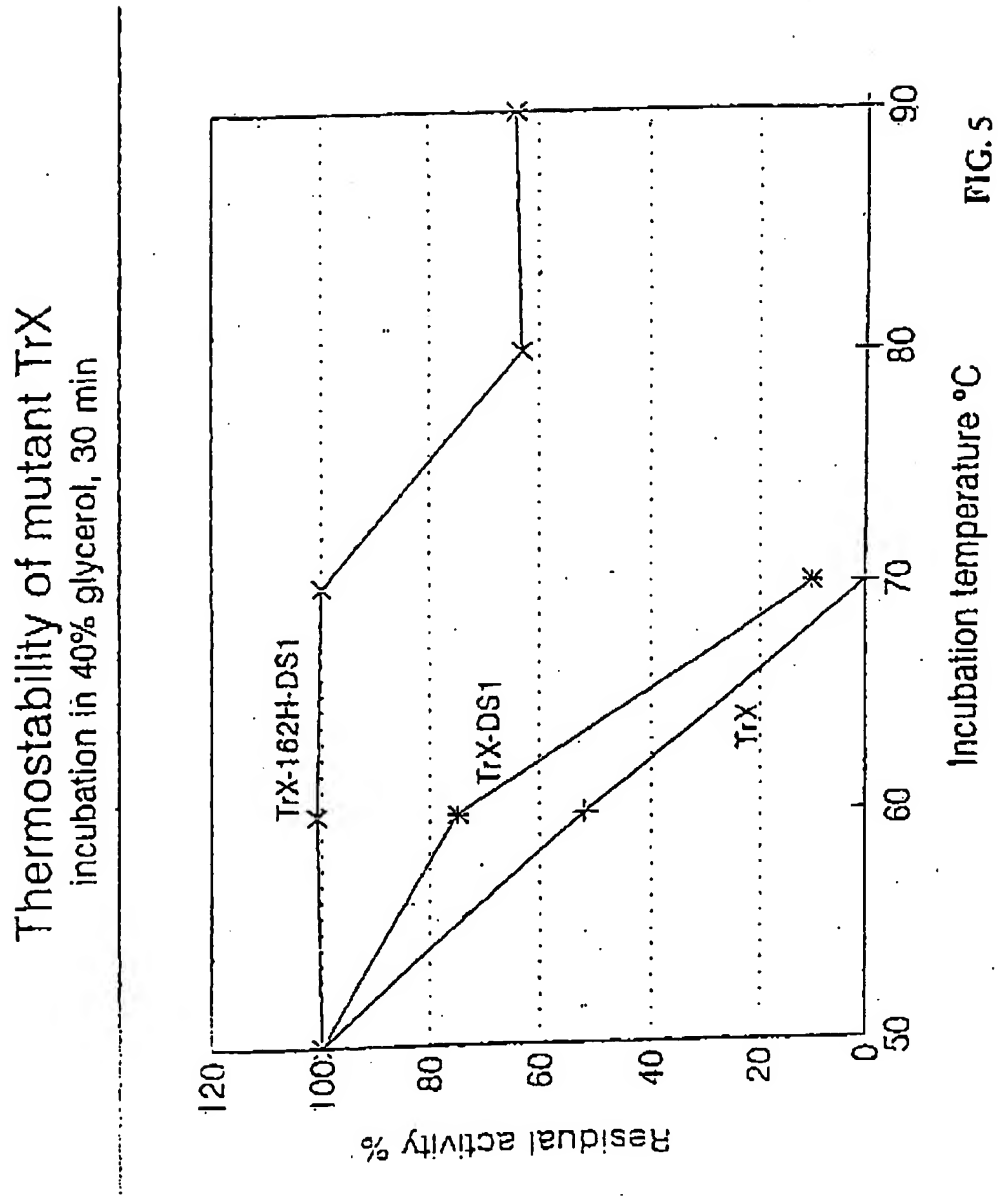
Thermostability of mutant TrX
incubation in 40% glycerol, 30 min
Residual activity %
120
100
80
60
40
20
0
50
60
70
80
90
Incubation temperature °C
TrX-162H-DS1
TrX-DS1
TrX

FIG. 5

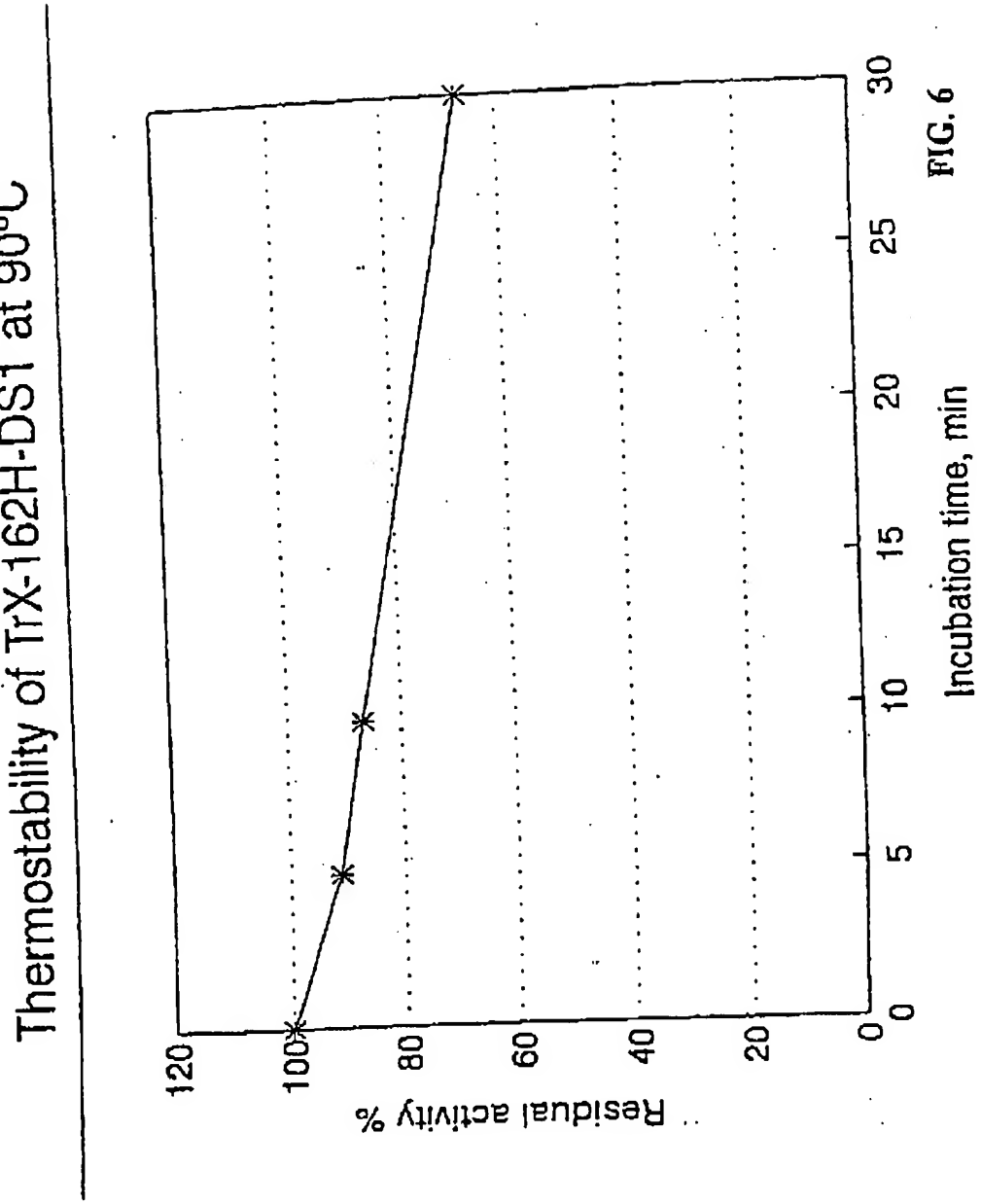

FIG. 6

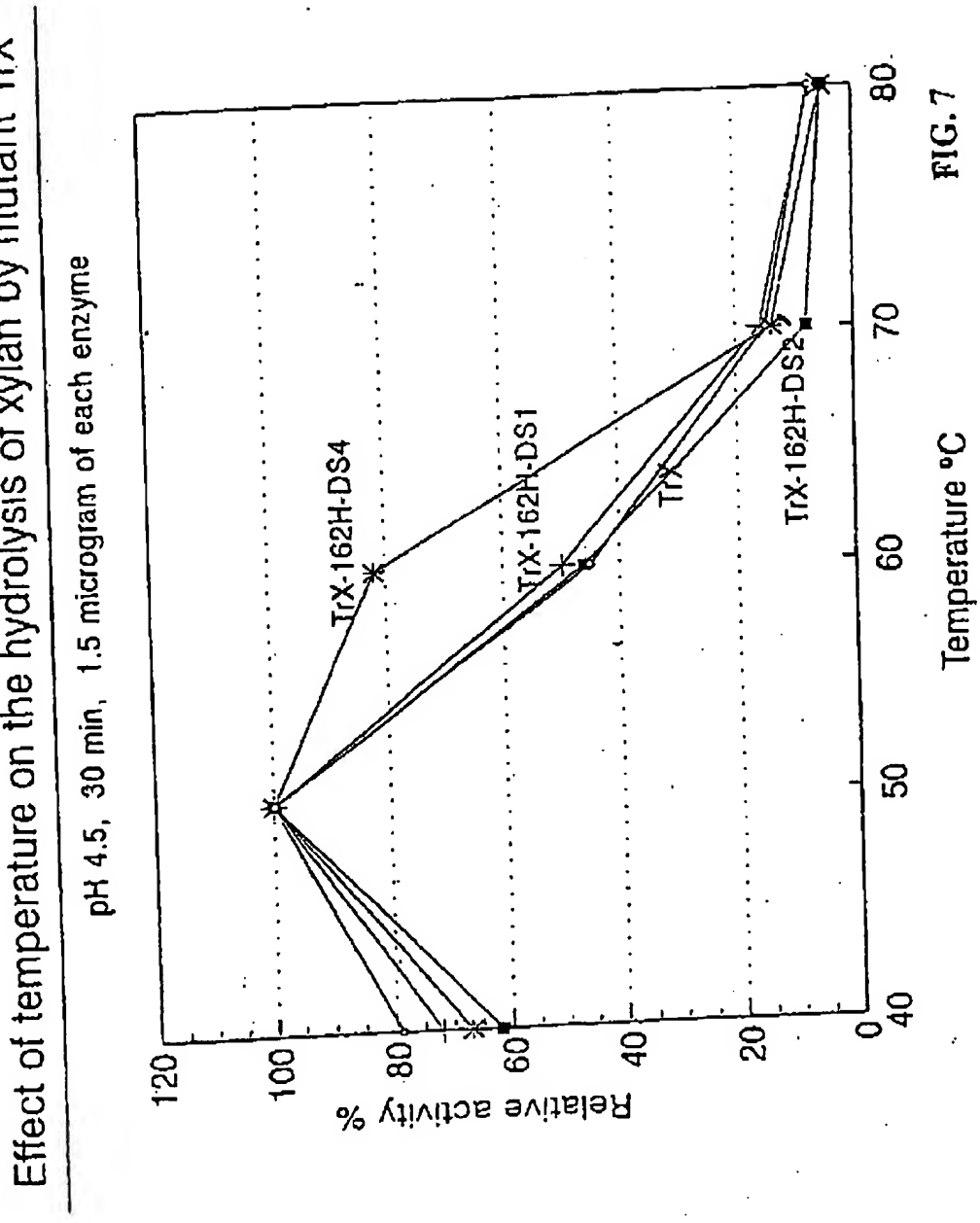
Effect of temperature on the hydrolysis of xylan by mutant TrX
pH 4.5, 30 min, 1.5 microgram of each enzyme
Relative activity %
120
100
80
60
40
20
0
40
50
60
70
80
Temperature °C
TrX-162H-DS4
TrX-162H-DS1
TrX
TrX-162H-DS2

FIG. 7

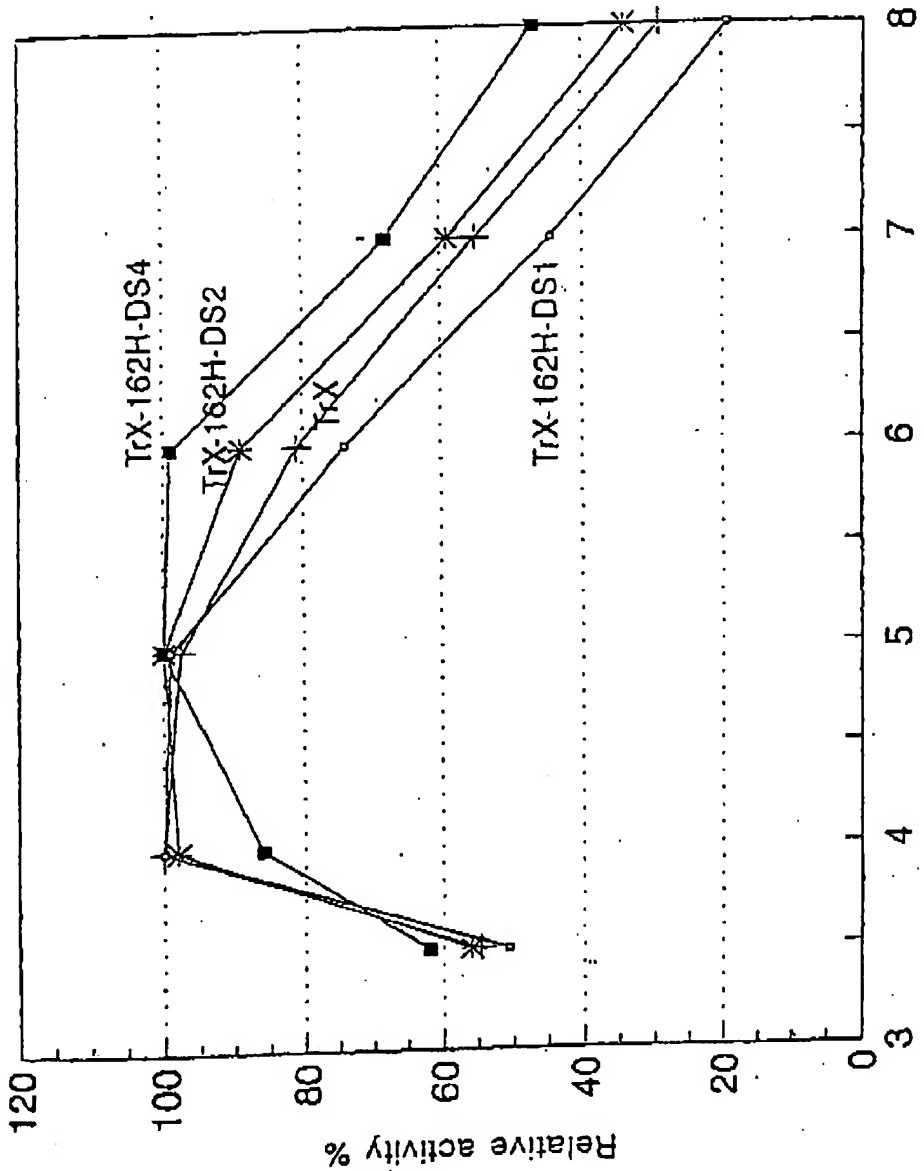

FIG. 8